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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2618.26 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-2

Perfect score: 1017
Sequence: 1 atgaagtctatctatctgc.....caggtgttccaagaataaa 1017

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
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31: em_hcg_inv:*
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35: em_hcg_rtd:*
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37: em_hcg_vrt:*
38: em_sv:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217.4	21.4	808	3	AB045178 Reticulit
2	217.4	21.4	828	3	AB045179 Reticulit
3	214.2	21.1	840	3	AB045172 Reticulit
4	211.8	20.8	714	3	AB045171 Reticulit
5	208.4	20.5	770	3	AB045170 Reticulit
6	204	20.1	780	3	AB045168 Reticulit
7	198.8	19.5	784	3	AB045167 Reticulit
8	196.4	19.3	781	3	AB045165 Reticulit
9	194.8	19.2	785	3	AB045177 Reticulit
10	194.4	19.1	759	3	AB045174 Reticulit
11	192.6	18.9	783	3	AB045173 Reticulit
12	191.2	18.8	802	3	AB045176 Reticulit
13	189.4	18.6	1443	8	FSOKCH
14	189.4	18.6	1473	6	A21795
15	189.4	18.6	1473	6	A23637
16	189.4	18.6	1473	6	A23646
17	189.4	18.6	1473	6	A23955
18	189.4	18.6	1473	6	A23959
19	189.4	18.6	1473	6	A41660
20	189.4	18.6	1473	6	AR072922
21	189.4	18.6	1473	6	BD002249
22	189.4	18.6	1473	6	BD010853
23	189.4	18.6	1473	6	I13885
24	189.4	18.6	1473	6	I21317
25	189.4	18.6	1473	6	I57984
26	188.4	18.5	761	3	AB045175 Reticulit
27	187.6	18.4	798	3	AB045166 Reticulit
28	186.2	18.3	785	3	AB045169 Reticulit
29	181.2	17.8	927	6	AR094307 Sequence
30	181.2	17.8	1423	6	AR094309 Sequence
31	181	17.8	960	6	AR094305 Sequence
32	180.8	17.8	919	6	A68072
33	180.8	17.8	919	6	AR163168 Sequence
34	180	17.7	894	6	AR094306 Sequence
35	178.8	17.6	924	6	A68074
36	178.8	17.6	924	6	AR163169 Sequence
37	173.8	17.1	1132	6	AR094315 Sequence
38	173.2	17.0	1418	8	AJ277482 P1omyces
39	169.6	16.7	922	6	A68070
40	169.6	16.7	922	6	AR163167 Sequence
41	165.4	16.3	1154	6	AR094308 Sequence
42	162.2	15.9	913	6	AR094311 Sequence
43	160.4	15.8	885	6	AR094316 Sequence
44	160	15.7	912	6	A68076
45	160	15.7	912	6	AR163170 Sequence

ALIGNMENTS

RESULT 1
AB045178 808 bp mRNA linear INV 14-FEB-2001
LOCUS AB045178
DEFINITION Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
ACCESSION AB045178
VERSION AB045178
KEYWORDS AB045178.1 GI:8926988
SOURCE Reticulitermes speratus hindgut symbiont 130484
ORGANISM Reticulitermes speratus hindgut symbiont 130484
REFERENCE 1 (sites)
AUTHORS Ohnoko,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family

Db 310 TGGAGGTGAGACTGAGCTTTGTCAGATTGCTATGAGCTTACGATGACAGAGTGGCCAGT 369
 Qy 687 TGTGTTAAGAAAGATGTTGTTCCAGTCACTAAGTGGTGGATCTTGGCTCTCTAC 746
 Db 370 GAATGAAAGAAAGATGTTGTTCCAGTCACTAAGTGGTGGATCTTGGCTCTCTAC 427
 Qy 747 TGTGTTAAGAAAGATGTTGTTCCAGTCACTAAGTGGTGGATCTTGGCTCTCTAC 806
 Db 428 -----CAATTGATCTTGCATTTCCAGAGAGAGGTTGGATTTCATGATGATGAC 480
 Qy 807 CAGCAATGGGGTGTCTCCATGATGAGCGTTGGGGCTCAGATGAGTGTATTTCTTCTC 866
 Db 481 TCAGCAATGAGGTCAGCTGTGATGATGAGGAGCGGTTATGAGTGTGTCATCTCG 540
 Qy 867 ATCTGACTCTTACTGTTCTTCTTCCGACTCCAGTGGTGTGAATGAGATTCACAG 926
 Db 541 TTCTGATGTTCTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
 Qy 927 GTTCAAGAGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 986
 Db 601 GTTCAAGAGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Qy 987 CACCGCAAGACAGGTTGTTCAAGAAATTA 1017
 Db 661 GATAGCAAGACCAATTGCAAGCTACTTA 691

RESULT 3
 AB045172 840 bp mRNA linear INV 14-FEB-2001
 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION AB045172
 ACCESSION AB045172 GI:8926976
 VERSION
 KEYWORDS Reticulitermes speratus hindgut symbiont 130484
 SOURCE
 ORGANISM
 REFERENCE 1 (sites)
 AUTHORS Ohkuma, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 840)
 AUTHORS Ohkuma, M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hirotsawa 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
 FEATURES
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BASE COUNT 227 a 157 c 200 g 256 t
 ORIGIN
 Query Match 21.1%; Score 214.2; DB 3; Length 840;

Best Local Similarity 62.3%; Pred. No. 5.5e-49;
 Matches 393; Conservative 0; Mismatches 223; Indels 15; Gaps 3;

Qy 390 TGTGTAAGGTGCTACTACTGTTATGAGATGCTGTAAGGCTCTGAGTGGCCCG 449
 Db 72 TGAATCTGGAGAGACACCGCTTACTGGAAGCTGTTGCAAGCTGCTGATGAGAAA 131
 Qy 450 TAAAGCAATGCTACTCTCTGTCATGCTCTGTAACAAAGATGCTACGCCCTT 507
 Db 132 AAAAGCTGCTGACTACAGCTCTGTCATGACATGCCAAAAGATGCAACAGAGTTGC 191
 Qy 508 -AGTACAGCAATGCTCCAAAGTGGCTGTAACGGTGTGTAACATGATGTAAGACAA 566
 Db 192 AAGCAATGCAAGGAAATCTGCTGTGATGATGATGATGATGATGATGATGATGATGAT 251
 Qy 567 CCAACCTGGGCTGTAACGACACACCTGCTATGCTTCTGCTGCTGCTGCTGCTGCTG 626
 Db 252 ACGACCTGGGCTGTAATGACTCGGTTGCAATACGTTTGGCTGCGAGC---TTGCTG 308
 Qy 627 TGTGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686
 Db 309 TGAAGCGAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 368
 Qy 687 TGTGTAAGAAAGATGTTGTTCCAGTCACTAAGTGGTGGATCTTGGCTCTCTAC 746
 Db 369 TATGGAAGAAAGATGTTGTTCCAGTCACTAAGTGGTGGATCTTGGCTCTCTAC 423
 Qy 747 TGTGCTCACTTGAAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
 Db 424 ---AATCAATTTGATCTTGCATATTCGCGAGAGAGGTGCGAATTTCAATGATGAC 479
 Qy 807 CAGCAATGGGGTGTCTCCAAATGAGCGTTGGGGCTCAAGATGAGGTGATTTCTTCTC 866
 Db 480 TCAACATGAGGGGGGCTCCGATGAGTGGGAGAACCGAATGAGGTGTTCACTG 539
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 Db 540 ATCTGATGTTCTCACTCTTCCATGAGTCTTCAAGCTGATGATGATGATGATGATGAT 599
 Qy 927 GTTCAAGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 986
 Db 600 GTTCAAGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 659
 Qy 987 CACCGCAAGACAGGTTGTTCAAGAAATTA 1017
 Db 660 GACGCAAGACCAATTGCAAGCTACTTA 690

RESULT 4
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 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION AB045171
 ACCESSION AB045171 GI:8926974
 VERSION
 KEYWORDS Reticulitermes speratus hindgut symbiont 130484
 SOURCE
 ORGANISM
 REFERENCE 1 (sites)
 AUTHORS Ohkuma, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 710)
 AUTHORS Ohkuma, M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hirotsawa 2-1, Wako-shi, Saitama 351-0198, Japan

(E-mail: mohkuma@mailman.riken.go.jp, Tel: 66-48-467-9545,
Fax: 66-48-462-4672)

FEATURES

Source

CDS

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ORIGIN				

Query Match	20.8%;	Score 211.8;	DB 3;	Length 710;
Best Local Similarity	62.2%;	Pred. No. 2.6e-48;		
Matches 350; Conservative	0;	Mismatches 222;	Indels 15;	Gaps 3.

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Db	65	AGCGGAAGAACACCCGGTATTGGGATTTTCCAAAGCCAGCTGTGCGTGGGAAAAAAA	124
QY	454	GCCATGTCACTTCTCTGTCAAGTCTGTMAAAGATGATGACATGCGCTT--AGT	510
Db	125	GCTGCTGTACACAGCGCTGTGACCTTGTGAAAAAGATGGGACACAGAGTGTCCGAGC	184
QY	511	GACAGCAATGCCCAAGTAGTGGCTGTAAAGGTGTGTACGTTAATGTGTAAACGAAACCA	570
Db	185	AATGACACTGTGAAATTCAGCTTGTGATGTGAGAAAGATATGTATTATATGACGA	244
QY	571	CTTTGGGCGTAAACGACAACTTGCTATAGTTTCGCTGCTGCTCCATCAGTGGTGT	630
Db	245	CCATGGGCGATTATATACCTCTGTGGCTAGCGTTTGTCTGCTGACG---TTCGTGTGG	301
QY	631	GGTGATCTCGCTGTGCTGTTCTTGTGTTGAACTTACTTTCACTTCACTCTGTGCT	690
Db	302	GGCGAAAGCGGAGCTTGCTGCATTTCTATGAGCTTACATTCACAAGTGAACAGTGAAT	361
QY	691	GGTAAAGATGTTGTCCAACTCATTAACATGGGTGATCTTGGCTCTCTATGGT	750
Db	362	GGAAAGAAATGTTGTATACAGTCACAAACCGGGTGGATCTTGGCTCGAA-----	414
QY	751	GCTCACTTTGACTTGCMAATGCCCGGTGTGTGTGTATTTCAATGATGTTTCCAGC	810
Db	415	--TCACTTTGATTTGCGATTCGGGTGGAGGTGTTGGGATCTACAAACGTTGCCACG	472
QY	811	CAATGGGGTGTCCCAATGACGTTGGGGCTCAAGATAGGTGTATTTCTTCTGATCT	870
Db	473	CAATCAGGTGCACTCTGTATGTATGGGAAAGCCGATATGGAAGTGTTCATCCGACG	532
QY	871	GACTGCTAGTCTTCTCTCGGACATCCAAAGCTGTGTATATAGGATTTCAACTGGTT	930
Db	533	GAATGCTTTCAGCTTCCGTGGGCTTCAAGCTGGGTCCCAATGAGATTTGATTTGGTTC	592
QY	931	AAGAACGCTGATTAACCCAGACATGACTTACAGGAAGTTACTGTCTTAAGAAATCACC	990
Db	593	CAAAATGCGGATTAACCTTCAATCAATTTCAACCAAGTGACATGCTCGTGTAGTTAACG	652
QY	991	GCCAAAGCAGGTTGTTCAAGAAAAATA	1017
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RESULT 5	AB045170	774 bp	mRNA	linear	INV 14-FEB-2001
LOCUS	AB045170				
DEFINITION	Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45				

ACCESSION AB045170 GI:8926972
VERSION AB045170.1

KEYWORDS
SOURCE
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA

clone:8-38.
ORGANISM Reticulitermes speratus hindgut symbiont 130484

REFERENCE

1 (sites)
Unclassified.

Obayama K. Obayama M. Moriya S. Inoue T. Usami R. and Kudo T.

45 diverse genes of cellulase homologues of glycosyl hydrolase family
46 from the symbiotic protists in the hindgut of the termite
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Reticulitermes speratus
Extremophiles 4 (6), 343-349 (2000)

MEDLINE 21020023
REFERENCE 2 (bases 1 to 774)

AUTHORS	Ohkuma, M.
TITLE	Direct Submission
Submitted (YY-MM-2000)	Moriya Ohkuma
FORNAT	RIKEN (The Institute of

2-1, Wako-shi, Saitama 351-0198, Japan

(E-mail: mohkuma@mailman.riken.go.jp, Tel: 66-48-467-9545
Fax: 66-48-462-4672)

FEATURES	Location/Qualifiers
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Best Local Similarity	61.7%	Pred. No.	2.4e-47;			

Matches	389;	Conservative	0;	Mismatches	226;	Indels	15;	Gaps	10
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391 GGTACCGGTCTCACTACTCGTATTGGGATTGCTGTAGGCTCCTGTAGTGGCCCC

Db 97 GATACCTGGCAGACACACCCGTATTGGGATTCTGGCAAGGAAGTGTGGCTGGAGAG

Dy 451 AAGGCCAAATGTCAGTCTCCIGICAMGICCGIACCAAGATGGTGATGCTCCTCC

508 AGTGCACGCAATGCCAAAGTGGCTGTAACGGTGTACAGTTACATGTGTAAAGAC

217 AGCAACGACACCGTTAAGTCAGGCTGTGATGCCGAGATGGATATATGTTATGAT

568 CAACCTTGGGCTGTAACGACAACCTTGCTATGCTTCGCTGCTGCCATCAGT

Db 277 TCTCCGTGGGCTGTCATGATCTTTTGGCTCTGGGTTTGTCTGCTGCAGCGGTTTCA

628 GGTGGTGAATCGCTGGGCTGTTCTTGTTCGAACCTACTTTCACCTCTCT

Db 337 GGTCAGAGCGCTGCC--TGTCGAATTGTTACGAGTTAACATTCACCTCTGGSCCA

688 GCTGTAAAGATGGTTGTCGAAGTCACTAACACTGCTGTGTAICTTGCTCTCT

Db 394 AATGAAAGATGACTGTTCAAGTTACCAACACTGGGGTGACTTGGTTC---

748 GGCTCACCATTGACCTGC AATGCCCGGTGGTGGTGTTGGTAATTC AAGTGTG
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Db 448 --AATCAGTTGATCTTGCATTCACGGTGGTGGTGGAACTACACCGGCTG

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 DB 505 GGCATCTGGTCTCTCTCTGATGATGGGAAAGTCGTTATGTTGTTCTCTCCCA 564
 QY 868 TCTGACTGCTTAGTCTTCTCTCCGACATCCAGCTGTTGTAATGAGATTCAATG 927
 DB 565 AGGATATGCTGACGCTTCGTCGGGACCTTCAGGCTGCGCAGGGGCTTTTGACTG 624
 QY 928 TTCAAGACGCTGATTAACCAAGCATGATCTTACCAAGAGTTACCTGCTCAAGAAATC 987
 DB 625 TTCCAGAAAGCTGATATATCCGTCATCAGCTTCAAGCGTGTTCGTCTCTAGTGAATTG 684
 QY 988 ACCGCCAGACAGGTTGTTCAAGAAATTA 1017
 DB 685 ATTGGCAAAACGACTGATGAGCTGTTTA 714

RESULT 6
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 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:4-44, complete cds.
 ACCESSION AB045168
 VERSION AB045168.1 GI:8926968
 KEYWORDS
 SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:4-44.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 Unclassified.
 REFERENCE 1 (sites)
 AUTHORS Ohoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 780)
 AUTHORS Ohkuma, M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hiroswawa 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

FEATURES
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 /clone="4-44"
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CDS
 155 c 206 g 223 t

BASE COUNT 196 a 155 c 206 g 223 t

ORIGIN
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 Best Local Similarity 61.2%; Pred. No. 4.1e-46;
 Matches 367; Conservative 0; Mismatches 230; Indels 15; Gaps 3;

QY 388 TCTGTACGCTGTCTACTCTGTTATTTGGATTGCTGTAGAGCCCTCTGTAGCTGCC 447
 DB 64 TGTGACAGTGGCAAAAGCAGCCGCTATTGGGACTGCTGCAAGGCTCTGTGGCTGGAA 123
 QY 448 GGTAGGCCAATGTCTCTCTGCAAGTCTGTGAACAAAGATGTGTCACTGACCTTT 507
 DB 124 GCCAAAGCTGATGTGACAAACCGATGACACGCTGGCAAAAGATGGACAACTCGATT 183

QY 508 AGTGACAGCAATGCCCAAG---TGGCTGAACGGTGTGAACGTTATCATGTGTACGAC 564
 DB 184 GGAAGCAAGATACAGTAAATCTGTTGTGTATGGCGGAGAGGCTGATGTGCTACGAT 243
 QY 565 AACCACTTGGGGCTGTAAACGACAACTTGGCTTATGTTTGGCTGCTGCTCATGCT 624
 DB 244 CAACCCCGTGGGGGTCAACCATTTCTTAAGGTTGGGATTTTGCTGCTCAGCAATTTCA 303
 QY 625 GGTGGGTGATATTCGGCTGGTCTTCTTTTGGAACTTACCTTGCACTTCTCTCT 684
 DB 304 GGAAGTGAGAGGCTGCC---TGGTATATTTATGAGATTACCTTCACTTGAGCCCC 360
 QY 685 GTTGTGTGAAGATGAGTGTGTCCAAAGTCACTTAACATGTGTGATTTGGCTCTCT 744
 DB 361 GTTATGGCAAAAGATGACTTGTTCAGTTACCAACCGGAGGATTCGCTT----- 416
 QY 745 ACTGCTGCTCACTTGTGCAAAATGCCGGTGTGTGTGTGTATTTTCAATGGTTGT 804
 DB 417 -----GAATCAATTTGATCTCGCCATTCCAGGTGGTGTGCGTATTATTAATGATGTC 471
 QY 805 TTCAGCAATGGGGTGTCTCCCAATGACGTTGGGGCTCAAGATACGTTATTTCTTCT 864
 DB 472 ACAGCTCAATCTGTGCTCTCTGCTGATGTTGGGAAGTCGGTATGAGAGGCTCTCTCC 531
 QY 865 GCATCTGACTGCTAGTCTTCTCTCCGACATCCAGCTGTTGTAATGAGATTCAAC 924
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 QY 925 TGGTTCAAGAACGCTGATTAACCAAGCATGACTTACAGAAAGTTAAGTCTGCTTAAGAA 984
 DB 592 TGGTTCAAAATAGCGACATCCGTCATGAATTAAGTGTGTCGTCGCCAGTGTAG 651
 QY 985 ATCACCAGCAAGACAGTGTGTTCAAGAAATA 1016
 DB 652 TTGATTGCAAAACCAATTGACAGCGCAATTA 683

RESULT 7
 AB045167 784 bp mRNA linear INV 14-FEB-2001
 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:8-16, complete cds.
 ACCESSION AB045167
 VERSION AB045167.1 GI:8926966
 KEYWORDS
 SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:8-16.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 Unclassified.
 REFERENCE 1 (sites)
 AUTHORS Ohoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 JOURNAL Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 784)
 AUTHORS Ohkuma, M.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hiroswawa 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)

FEATURES
 source Location/Qualifiers
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 RN"

ORIGIN

202 a 153 c 210 g 219 t

Query Match

19.5%: Score 198.8; DB 3; Length 784;
 Best Local Similarity 60.8%; Pred. No. 1.2e-44;
 Matches 383; Conservative 0; Mismatches 232; Indels 15; Gaps 3;

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 309 AGAAGCGCAAAAGCGCGATGCTGCACTGTAAAGTGTGTATGCTGCTGCTGCTGCT 368
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 987 CACCGCCAGACAGGTTGTCAAGAAATA 1016
 660 GATTGCAAAACCAATTTGACAGCAATTA 689

RESULT 8
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 LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
 DEFINITION cellulase homologue, clone:2-54, complete cds.
 ACCESSION AB045165
 VERSION AB045165.1 GI:8926962
 KEYWORDS Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
 clone:2-54.
 SOURCE Reticulitermes speratus hindgut symbiont 130484
 ORGANISM Unclassified.
 REFERENCE 1 (sites)
 AUTHORS Ohkuma,K., Ohkuma,M., Moriya,S., Inoue,T., Usami,R. and Kudo,T.
 TITLE Diverse genes of cellulase homologues of glycosyl hydrolase family

JOURNAL

45 from the symbiotic protists in the hindgut of the termite
 Reticulitermes speratus
 Extremophiles 4 (6), 343-349 (2000)
 MEDLINE 21020023
 REFERENCE 2 (bases 1 to 781)
 AUTHORS Ohkuma,M.
 TITLE Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
 Physical and Chemical Research), Microbiology Laboratory; Hirotsawa
 2-1, Wako-shi, Saitama 351-0198, Japan
 (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
 Fax:66-48-462-4672)

FEATURES

source

CDS

BASE COUNT

193 a 143 c 210 g 235 t

ORIGIN

Query Match 19.3%; Score 196.4; DB 3; Length 781;
 Best Local Similarity 61.0%; Pred. No. 5.6e-44;
 Matches 377; Conservative 0; Mismatches 226; Indels 15; Gaps 3;

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 463 AGTTCTGCTCAAGTCTGTAAACAAGTGTGTACAGCCCT--AGTACAGCAAT 519
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QY 1000 GGTTGTCAGAAATAA 1017
 DB 670 AATGCAACGTAATTAA 687

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 DEFINITION cellulase homologue, clone:1-14, complete cds.
 AB045177
 VERSION AB045177.1 GI:8926986
 KEYWORDS
 SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:1-14.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 UNCLASSIFIED.
 REFERENCE 1 (sites)
 Ohoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 Extremophiles 4 (6), 343-349 (2000)
 JOURNAL 21020023
 MEDLINE 2 (bases 1 to 785)
 REFERENCE Ohkuma, M.
 AUTHORS Direct Submission
 TITLE Submitted (24-JUN-2000) Moriya, Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hirotsawa 2-1, Wako-shi, Saitama 351-0198, Japan
 JOURNAL (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
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 Matches 376; Conservative 0; Mismatches 227; Indels 15; Gaps 3;

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 QY 463 AGTTCTCTGTCAGCTGTAAACAAGATGCTGACCTCTT---AGTGACAGCAAT 519
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DB 318 GGTGCTGCTGTGCTGCTATGATTTGACATTCACAGTGGCCCGGTCAACCGAAGCAT 377
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 QY 760 GACTTGCAAAATGCCGGTGTGTGTGTATTTTCAATAGTTTTCAGCCATGGGT 819
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 QY 940 GATACCCAGACATCTTACAGAGGATTAACCTGTCTTACAGAAATCACCCCAAGACA 999
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RESULT 10
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 DEFINITION cellulase homologue, clone:1-1, complete cds.
 AB045174
 VERSION AB045174.1 GI:8926980
 KEYWORDS
 SOURCE Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA, clone:1-1.
 ORGANISM Reticulitermes speratus hindgut symbiont 130484
 UNCLASSIFIED.
 REFERENCE 1 (sites)
 Ohoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 Diverse genes of cellulase homologues of glycosyl hydrolase family 45 from the symbiotic protists in the hindgut of the termite Reticulitermes speratus
 Extremophiles 4 (6), 343-349 (2000)
 JOURNAL 21020023
 MEDLINE 2 (bases 1 to 759)
 REFERENCE Ohkuma, M.
 AUTHORS Direct Submission
 TITLE Submitted (24-JUN-2000) Moriya, Ohkuma, RIKEN (The Institute of Physical and Chemical Research), Microbiology Laboratory, Hirotsawa 2-1, Wako-shi, Saitama 351-0198, Japan
 JOURNAL (E-mail:mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545, Fax:66-48-462-4672)
 FEATURES
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BASE COUNT 194 a 133 c 208 g 224 t
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Query Match 19.1%; Score 194.4; DB 3; Length 759;

Best Local Similarity 60.3%; Pred. No. 2e-43;
Matches 381; Conservative 0; Mismatches 236; Indels 15; Gaps 3;

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Db 116 AGAAGGCCAATGTGACAAAGCCATTGATACATGTGCAAAAGATGCGTCAAGAGTGG 175
QY 508 -AGTACAGCAATGCCCAGCAAGTGTGCTGTAACGGTGTGTAACATGATGTGAAGACA 565
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RESULT 11
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LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
DEFINITION cellulase homologue, clone:7-10, complete cds.
ACCESSION AB045173.1 GI:8926978
VERSION
KEYWORDS
SOURCE
ORGANISM
Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA,
clone:7-10.
Reticulitermes speratus hindgut symbiont 130484
Unclassified.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
2-1, Wako-shi, Saitama 351-0198, Japan

FEATURES
source
Location/Qualifiers
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BASE COUNT 201 a 150 c 209 g 223 t
ORIGIN

Query Match 18.9%; Score 192.6; DB 3; Length 783;
Best Local Similarity 60.6%; Pred. No. 6.5e-43;
Matches 375; Conservative 0; Mismatches 229; Indels 15; Gaps 3;

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QY 986 TCACCGCCAAAGCAGTTG 1004
Db 662 TTAATGCTAAACCAATTG 680

RESULT 12
AB045176 802 bp mRNA linear INV 14-FEB-2001
LOCUS Reticulitermes speratus hindgut symbiont 130484 mRNA for family 45
DEFINITION

cellulase homologue, clone:1-16, complete cds.
 AB045176
 GI:8926984
 Reticulitermes speratus hindgut symbiont 130484 cDNA to mRNA.
 clone:1-16.
 Reticulitermes speratus hindgut symbiont 130484
 Unclasseified.
 1 (sites)
 Ohoko, K., Ohkuma, M., Moriya, S., Inoue, T., Usami, R. and Kudo, T.
 Diverse genes of cellulase homologues of glycosyl hydrolase family
 45 from the symbiotic protists in the hindgut of the termite
 Reticulitermes speratus
 Extremophiles 4 (6), 343-349 (2000)
 21020023
 2 (bases 1 to 802)
 Ohkuma, M.
 Direct Submission
 Submitted (24-JUN-2000) Moriya Ohkuma, RIKEN (The Institute of
 Physical and Chemical Research), Microbiology Laboratory, Hiroshima
 2-1, Mako-shi, Saitama 351-0198, Japan
 (E-mail: mohkuma@mailman.riken.go.jp, Tel:66-48-467-9545,
 Fax:66-48-462-4672)
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 V"
 BASE COUNT 195 a 155 c 219 g 233 t
 ORIGIN
 Query Match 18.8%; Score 191.2; DB 3; Length 802;
 Best Local Similarity 60.0%; Pred. No. 1.6e-42;
 Matches 379; Conservative 0; Mismatches 238; Indels 15; Gaps 3;
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 QY 926 GGTTCAGAACGCTGATATACCAAGATGATCTTACAGGAATTTCTGCTTAAGGAA 985
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 DB 688 TTATTGCCAAAACCATTTGCAACCGAGTTAA 719
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 LOCUS
 DEFINITION Fusarium oxysporum K-family cellulase homologue mRNA, complete cds.
 ACCESSION L29381
 VERSION L29381.1 GI:520822
 KEYWORDS K-family cellulase homologue; cellulase; homologue.
 SOURCE Fusarium oxysporum cDNA to mRNA.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.
 1 (bases 1 to 1443)
 SHEPPARD, P.O., Grant, F.J., Oort, P.J., Sprecher, C.A., Foster, D.C.,
 Hagen, F.S., Upshall, A., McKnight, G.L. and O'Hara, P.J.
 The use of conserved cellulase family-specific sequences to clone
 cellulase homologue cDNAs from Fusarium oxysporum
 Gene 150 (1), 163-167 (1994)
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 JOURNAL MEDLINE PUBMED
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 Query Match 18.6%; Score 189.4; DB 8; Length 1443;
 Best Local Similarity 59.0%; Pred. No. 5.1e-42;
 Matches 369; Conservative 0; Mismatches 241; Indels 15; Gaps 2;
 QY 380 GTGGTCTCTGTTGAACGCTGCTACTCTGTTATTTGGATGCTGTAGAGCTCCTGTA 439
 DB 129 GTGGTCTCTTGTGAAGCGGTCACTACTCGATCTGGGATTTGTCGAACCTTTCTTGT 188
 QY 440 GCTGACCGCGTAAGGCCAATGTCACTTCTCTGTCAGTCTGTAAAGTGAAGTGTGTA 499
 DB 189 CTGGAAGCGGAAGGCTGTGTCAACGCCCTTCTTAATCTGTGTAAAGACCAAC 248
 QY 500 CTGCCCTTAGTACAGCAATGCGCAAGTGTGCTGAACGCTGTGAACAGTTACATGTGTA 559
 DB 249 CATTTCACAAACCAATGCTGTCAACGCTGTGAGAGGTGTGTTCTGCTTATGTGCTGCA 308

RESULT 14			
A21795	A21795	1473 bp	mRNA linear PAT 20-SEP-1995
LOCUS			
DEFINITION	F. oxysporum mRNA for endonuclease component.		
ACCESSION	A21795		
VERSION	A21795.1	GI:1246874	

Query Match	18.6%	Score 189.4	DB 6	Length 1473
Best Local Similarity	59.0%	Pred. No. 5,1e-42		
Matches 369; Conservative	0	Mismatches 241	Indels 15	Gaps 2

QY 380 GTGGTCCTGTGTAACGGTGCATCTGTTATGGAGTTCCTGAAGCCCTGTGA 439
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 GTCCTGTTTGAAAGGTCACCTACTGATATACGGATTGCTCAAGCCTTTCGT 202

RESULT 15			
A23637	1473 bp	mRNA	linear
LOCUS			
DEFINITION	F. oxysporum endoglucanase gene.		
ACCESSION	A23637		
VERSION	A23637.1 GI:832888		
KEYWORDS	endoglucanase.		
SOURCE	Fusarium oxysporum.		
PART	19-SEP-1991		

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ORGANISM      Fusarium oxysporum  
               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
               Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum  
               complex.  
REFERENCE     1 (bases 1 to 1473)  
AUTHORS       Convente,A.C., Busch,A. and Baeck,A.C.  
TITLE         Detergent compositions with high activity cellulase and softening  
              clays  
JOURNAL        Patent: EP 0495258-A 3 22-JUL-1992;  
              THE PROCTER & GAMBLE COMPANY  
FEATURES      Location/Qualifiers  
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BASE COUNT      343 a      453 c      337 g      340 t
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